

P200301025DK SEQ listing.ST25  
 SEQUENCE LISTING

<110> Copenhagen University Tech Trans Enheden  
 Mundy, John

<120> Plant disease resistance and SAR regulator protein

<130> P200301025

<160> 28

<170> PatentIn version 3.2

<210> 1

<211> 669

<212> DNA

<213> Arabidopsis sp.

<220>

<221> CDS

<222> (1)..(669)

<400> 1

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |    |
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| atg | gat | ccg | tcg | gag | tat | ttt | gcc | ggc | ggc | aat | cct | tcc | gat | caa | cag |  | 48 |
| Met | Asp | Pro | Ser | Glu | Tyr | Phe | Ala | Gly | Gly | Asn | Pro | Ser | Asp | Gln | Gln |  |    |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |   |  |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|---|--|----|
| aac | cag | aag | cg  | cg  | c   | tt  | c   | ag  | at  | t   | gt  | gt  | c   | c   | t   | c |  | 96 |
| Asn | Gln | Lys | Arg | Gln | Leu | Gln | Ile | Cys | Gly | Pro | Arg | Pro | Ser | Pro | Leu |   |  |    |
| 20  |     |     |     | 25  |     |     |     |     |     |     |     |     | 30  |     |     |   |  |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| agt | gtt | cac | aaa | gac | tct | cac | aaa | atc | aag | aaa | cct | cca | aaa | cac | cct |  | 144 |
| Ser | Val | His | Lys | Asp | Ser | His | Lys | Ile | Lys | Lys | Pro | Pro | Lys | His | Pro |  |     |
| 35  |     |     |     | 40  |     |     |     |     |     |     |     |     | 45  |     |     |  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| gcg | ccg | ccg | cca | aat | cgt | gac | caa | ccg | ccg | ccg | tat | att | cct | aga | gag |  | 192 |
| Ala | Pro | Pro | Pro | Asn | Arg | Asp | Gln | Pro | Pro | Pro | Tyr | Ile | Pro | Arg | Glu |  |     |
| 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |     |  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| ccg | gtg | gtt | atc | tac | gcc | gta | tcc | ccc | aag | gtt | gta | cac | gca | acc | gct |  | 240 |
| Pro | Val | Val | Ile | Tyr | Ala | Val | Ser | Pro | Lys | Val | Val | His | Ala | Thr | Ala |  |     |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| tct | gag | ttc | atg | aa  | gta | gtc | cag | cga | ctc | aca | ggg | atc | tcc | tct | ggt |  | 288 |
| Ser | Glu | Phe | Met | Asn | Val | Val | Gln | Arg | Leu | Thr | Gly | Ile | Ser | Ser | Gly |  |     |
| 85  |     |     |     | 90  |     |     |     |     |     |     |     |     |     | 95  |     |  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| gtt | ttc | ctc | gaa | tct | ggc | ggc | ggt | gga | gat | gtt | tca | ccg | gct | gct | agg |  | 336 |
| Val | Phe | Leu | Glu | Ser | Gly | Gly | Gly | Gly | Asp | Val | Ser | Pro | Ala | Ala | Arg |  |     |
| 100 |     |     |     | 105 |     |     |     |     |     |     |     |     | 110 |     |     |  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| cta | gct | tcc | acg | gaa | aat | gct | agt | cca | aga | gga | gga | aaa | gaa | ccg | gct |  | 384 |
| Leu | Ala | Ser | Thr | Glu | Asn | Ala | Ser | Pro | Arg | Gly | Gly | Lys | Glu | Pro | Ala |  |     |
| 115 |     |     |     | 120 |     |     |     |     |     |     |     | 125 |     |     |     |  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| gct | aga | gat | gag | acg | gtg | gaa | atc | aa  | ccg | gct | atg | gaa | gaa | gca | gct |  | 432 |
| Ala | Arg | Asp | Glu | Thr | Val | Glu | Ile | Asn | Thr | Ala | Met | Glu | Glu | Ala | Ala |  |     |
| 130 |     |     |     | 135 |     |     |     |     |     |     | 140 |     |     |     |     |  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| gaa | ttt | ggt | ggt | tat | gct | ccg | gga | ata | ctc | tcg | cca | tct | ccg | gcc | ttg |  | 480 |
| Glu | Phe | Gly | Gly | Tyr | Ala | Pro | Gly | Ile | Leu | Ser | Pro | Ser | Pro | Ala | Leu |  |     |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| ttg | cca | aca | gct | tct | acc | ggg | ata | ttc | tct | ccg | atg | tat | cat | caa | ggt |  | 528 |
| Leu | Pro | Thr | Ala | Ser | Thr | Gly | Ile | Phe | Ser | Pro | Met | Tyr | His | Gln | Gly |  |     |
| 165 |     |     |     | 170 |     |     |     |     |     |     |     |     | 175 |     |     |  |     |

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ggg atg ttt tcg ccg gct ata cca ctg gga tta ttc tcg ccg gcg gga  
 Gly Met Phe Ser Pro Ala Ile Pro Leu Gly Leu Phe Ser Pro Ala Gly  
 180 185 190

ttt atg agc ccg ttt cga agt cct ggc ttt act agt ttg gta gct tca  
 Phe Met Ser Pro Phe Arg Ser Pro Gly Phe Thr Ser Leu Val Ala Ser  
 195 200 205

cca act ttt gct gat ttc ttt agt cat att tgg gat caa gat tag  
 Pro Thr Phe Ala Asp Phe Phe Ser His Ile Trp Asp Gln Asp  
 210 215 220

<210> 2

<211> 222

<212> PRT

<213> Arabidopsis sp.

<400> 2

Met Asp Pro Ser Glu Tyr Phe Ala Gly Gly Asn Pro Ser Asp Gln Gln  
 1 5 10 15

Asn Gln Lys Arg Gln Leu Gln Ile Cys Gly Pro Arg Pro Ser Pro Leu  
 20 25 30

Ser Val His Lys Asp Ser His Lys Ile Lys Lys Pro Pro Lys His Pro  
 35 40 45

Ala Pro Pro Pro Asn Arg Asp Gln Pro Pro Pro Tyr Ile Pro Arg Glu  
 50 55 60

Pro Val Val Ile Tyr Ala Val Ser Pro Lys Val Val His Ala Thr Ala  
 65 70 75 80

Ser Glu Phe Met Asn Val Val Gln Arg Leu Thr Gly Ile Ser Ser Gly  
 85 90 95

Val Phe Leu Glu Ser Gly Gly Gly Asp Val Ser Pro Ala Ala Arg  
 100 105 110

Leu Ala Ser Thr Glu Asn Ala Ser Pro Arg Gly Gly Lys Glu Pro Ala  
 115 120 125

Ala Arg Asp Glu Thr Val Glu Ile Asn Thr Ala Met Glu Glu Ala Ala  
 130 135 140

Glu Phe Gly Gly Tyr Ala Pro Gly Ile Leu Ser Pro Ser Pro Ala Leu  
 145 150 155 160

Leu Pro Thr Ala Ser Thr Gly Ile Phe Ser Pro Met Tyr His Gln Gly  
 165 170 175

Gly Met Phe Ser Pro Ala Ile Pro Leu Gly Leu Phe Ser Pro Ala Gly  
 180 185 190

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Phe Met Ser Pro Phe Arg Ser Pro Gly Phe Thr Ser Leu Val Ala Ser  
 195 200 205

Pro Thr Phe Ala Asp Phe Phe Ser His Ile Trp Asp Gln Asp  
 210 215 220

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16

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<400> 4  
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16

<210> 5  
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 <213> Arabidopsis sp.

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 <222> (1)..(720)

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 Met Asp Asn Arg Ser Pro Arg Ser Arg Gly Ile Leu Gly Pro Arg Pro  
 1 5 10 15

48

ata cca ttg aaa gtc cgt gga gat tcg cac aag atc atc aag aag cca  
 Ile Pro Leu Lys Val Arg Gly Asp Ser His Lys Ile Ile Lys Lys Pro  
 20 25 30

96

cca cta gcg ccg cca cac ccg caa cca caa cca cca caa acc cat cag  
 Pro Leu Ala Pro Pro His Pro Gln Pro Gln Pro Pro Gln Thr His Gln  
 35 40 45

144

caa gaa ccg tca caa tcg ccg cca cct ggt ccc gtg att ata tac  
 Gln Glu Pro Ser Gln Ser Arg Pro Pro Pro Gly Pro Val Ile Ile Tyr  
 50 55 60

192

aca gta tct ccc agg att atc cat aca cac cct aat aac ttc atg aca  
 Thr Val Ser Pro Arg Ile Ile His Thr His Pro Asn Asn Phe Met Thr  
 65 70 75 80

240

ttg gtc caa cgt ctc aca ggt aaa acc tcc acc tcc aca aca tcc tcc  
 Leu Val Gln Arg Leu Thr Gly Lys Thr Ser Thr Ser Thr Thr Ser Ser  
 85 90 95

288

tcc tat tct tca tct acg tca gca cca aaa gac gcg tca aca atg gtt  
 Ser Tyr Ser Ser Thr Ser Ala Pro Lys Asp Ala Ser Thr Met Val  
 100 105 110

336

gat aca tct cat ggg ttg ata tct ccg gcg gct cgg ttt gct gtt aca  
 Asp Thr Ser His Gly Leu Ile Ser Pro Ala Ala Arg Phe Ala Val Thr  
 115 120 125

384

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|                                                                                                                                                               |     |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| gag aag gct aat atc tca aac gaa cta ggg aca ttt gtt gga ggc gaa<br>Glu Lys Ala Asn Ile Ser Asn Glu Leu Gly Thr Phe Val Gly Gly Glu<br>130 135 140             | 432 |
| ggg act atg gat caa tat tat cat tat cat cat cat cat cat caa<br>Gly Thr Met Asp Gln Tyr Tyr His His His His His His His Gln<br>145 150 155 160                 | 480 |
| gaa caa caa cat caa aat caa ggg ttc gag cg <sup>g</sup> cca agt ttc cac cat<br>Glu Gln Gln His Gln Asn Gln Gly Phe Glu Arg Pro Ser Phe His His<br>165 170 175 | 528 |
| gct ggg att tta tcg ccg gga cct aat tct ctg ccg tcg gta tca ccg<br>Ala Gly Ile Leu Ser Pro Gly Pro Asn Ser Leu Pro Ser Val Ser Pro<br>180 185 190             | 576 |
| gac ttc ttt tcc act att gga cca acc gat cca caa ggt ttt tcg tcg<br>Asp Phe Ser Thr Ile Gly Pro Thr Asp Pro Gln Gly Phe Ser Ser<br>195 200 205                 | 624 |
| ttc ttt aat gac ttt aac tct atc ctt cag agt agt cca tcg aag att<br>Phe Phe Asn Asp Phe Asn Ser Ile Leu Gln Ser Ser Pro Ser Lys Ile<br>210 215 220             | 672 |
| cag tct cct tct tct atg gac ctt ttc aac aat ttc ttt gat tct tga<br>Gln Ser Pro Ser Ser Met Asp Leu Phe Asn Asn Phe Phe Asp Ser<br>225 230 235                 | 720 |
| <210> 6<br><211> 239<br><212> PRT<br><213> Arabidopsis sp.                                                                                                    |     |
| <400> 6                                                                                                                                                       |     |
| Met Asp Asn Arg Ser Pro Arg Ser Arg Gly Ile Leu Gly Pro Arg Pro<br>1 5 10 15                                                                                  |     |
| Ile Pro Leu Lys Val Arg Gly Asp Ser His Lys Ile Ile Lys Lys Pro<br>20 25 30                                                                                   |     |
| Pro Leu Ala Pro Pro His Pro Gln Pro Gln Pro Pro Gln Thr His Gln<br>35 40 45                                                                                   |     |
| Gln Glu Pro Ser Gln Ser Arg Pro Pro Pro Gly Pro Val Ile Ile Tyr<br>50 55 60                                                                                   |     |
| Thr Val Ser Pro Arg Ile Ile His Thr His Pro Asn Asn Phe Met Thr<br>65 70 75 80                                                                                |     |
| Leu Val Gln Arg Leu Thr Gly Lys Thr Ser Thr Ser Thr Thr Ser Ser<br>85 90 95                                                                                   |     |
| Ser Tyr Ser Ser Ser Thr Ser Ala Pro Lys Asp Ala Ser Thr Met Val<br>100 105 110                                                                                |     |
| Asp Thr Ser His Gly Leu Ile Ser Pro Ala Ala Arg Phe Ala Val Thr<br>115 120 125                                                                                |     |

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Glu Lys Ala Asn Ile Ser Asn Glu Leu Gly Thr Phe Val Gly Gly Glu  
 130 135 140

Gly Thr Met Asp Gln Tyr Tyr His His His His His His His Gln  
 145 150 155 160

Glu Gln Gln His Gln Asn Gln Gly Phe Glu Arg Pro Ser Phe His His  
 165 170 175

Ala Gly Ile Leu Ser Pro Gly Pro Asn Ser Leu Pro Ser Val Ser Pro  
 180 185 190

Asp Phe Phe Ser Thr Ile Gly Pro Thr Asp Pro Gln Gly Phe Ser Ser  
 195 200 205

Phe Phe Asn Asp Phe Asn Ser Ile Leu Gln Ser Ser Pro Ser Lys Ile  
 210 215 220

Gln Ser Pro Ser Ser Met Asp Leu Phe Asn Asn Phe Phe Asp Ser  
 225 230 235

<210> 7  
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 <212> DNA  
 <213> *Arabidopsis sp.*

<400> 7  
 atggataata gatcgccaag

20

<210> 8  
 <211> 21  
 <212> DNA  
 <213> *Arabidopsis sp.*

<400> 8  
 tcaagaatca aagaaattgt t

21

<210> 9  
 <211> 791  
 <212> DNA  
 <213> *Brassica oleracea*

<220>  
 <221> CDS  
 <222> (139)..(789)

<400> 9  
 taatttttcc ctttttttt tgtttataaa tgtttggtc aatactagct cgtcgtcgac 60  
 aaagattcat ttcgattccc aaaccacaca agaagaacac aaatttagctc gaaagaaaca 120  
 aactcttttg agaaaata atg gat ccg tcg gag tct ttc gcc ggc ggc aat 171  
 Met Asp Pro Ser Glu Ser Phe Ala Gly Gly Asn  
 1 5 10

cct tcc gac caa cag aac cag aaa cgt cag ctt cag atc tgt ggt cct 219  
 Pro Ser Asp Gln Gln Asn Gln Lys Arg Gln Leu Gln Ile Cys Gly Pro

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| 15                                                                                                                                 | 20  | 25  |     |
|------------------------------------------------------------------------------------------------------------------------------------|-----|-----|-----|
| cgt ccc tca cct ctc agc gtc aac aaa gac tct cac aag atc aag aaa<br>Arg Pro Ser Pro Leu Ser Val Asn Lys Asp Ser His Lys Ile Lys Lys | 30  | 35  | 267 |
|                                                                                                                                    |     | 40  |     |
| cct cct aaa cac cct gct cct ccg cct cag cat cgc gac caa gct ccg<br>Pro Pro Lys His Pro Ala Pro Pro Pro Gln His Arg Asp Gln Ala Pro | 45  | 50  | 315 |
|                                                                                                                                    |     | 55  |     |
| ctc tac gct gct cga gag ccg gtg gtc atc tac gcc gtc tcg ccg aaa<br>Leu Tyr Ala Ala Arg Glu Pro Val Val Ile Tyr Ala Val Ser Pro Lys | 60  | 65  | 363 |
|                                                                                                                                    |     | 70  |     |
|                                                                                                                                    |     | 75  |     |
| gtc gtc cac acc aca gcc tcg gat ttc atg aac gtc gtc cag cgt ctc<br>Val Val His Thr Thr Ala Ser Asp Phe Met Asn Val Val Gln Arg Leu | 80  | 85  | 411 |
|                                                                                                                                    |     | 90  |     |
| acc ggc atc tca tcc gcc gtc ttc ctc gaa tcc ggt aac ggc gga gat<br>Thr Gly Ile Ser Ser Ala Val Phe Leu Glu Ser Gly Asn Gly Gly Asp | 95  | 100 | 459 |
|                                                                                                                                    |     | 105 |     |
| gta tct ccg gcg gcg aga ctc gcc gcg acc gag aat gca agc ccg aga<br>Val Ser Pro Ala Ala Arg Leu Ala Ala Thr Glu Asn Ala Ser Pro Arg | 110 | 115 | 507 |
|                                                                                                                                    |     | 120 |     |
| gga gga aaa gaa ccg gtg atg gcg gct aaa gat gag acg gtg gaa atc<br>Gly Gly Lys Glu Pro Val Met Ala Ala Lys Asp Glu Thr Val Glu Ile | 125 | 130 | 555 |
|                                                                                                                                    |     | 135 |     |
| gcg acg gct atg gaa gaa gca gcc gag ttg agc ggc tat gcg ccg ggg<br>Ala Thr Ala Met Glu Glu Ala Ala Glu Leu Ser Gly Tyr Ala Pro Gly | 140 | 145 | 603 |
|                                                                                                                                    |     | 150 |     |
| ata ctc tcc cct tct ccg gct atg tta ccg aca gct tct gcc gga ata<br>Ile Leu Ser Pro Ser Pro Ala Met Leu Pro Thr Ala Ser Ala Gly Ile | 160 | 165 | 651 |
|                                                                                                                                    |     | 170 |     |
| ttc tcg cag atg act act cac caa ggt ggg atg ttc tcg ccg gga ttg<br>Phe Ser Gln Met Thr Thr His Gln Gly Gly Met Phe Ser Pro Gly Leu | 175 | 180 | 699 |
|                                                                                                                                    |     | 185 |     |
| ttt tcg ccg gcg ggg tta atg agc ccg ttt ggt ttt gct agc ttg gtt<br>Phe Ser Pro Ala Gly Leu Met Ser Pro Phe Gly Phe Ala Ser Leu Val | 190 | 195 | 747 |
|                                                                                                                                    |     | 200 |     |
| gct tct cca acg ttt gct gat ttg ttc agt cat att tgg gga ta<br>Ala Ser Pro Thr Phe Ala Asp Leu Phe Ser His Ile Trp Gly              | 205 | 210 | 791 |
|                                                                                                                                    |     | 215 |     |
| <210> 10                                                                                                                           |     |     |     |
| <211> 217                                                                                                                          |     |     |     |
| <212> PRT                                                                                                                          |     |     |     |
| <213> Brassica oleracea                                                                                                            |     |     |     |
| <400> 10                                                                                                                           |     |     |     |
| Met Asp Pro Ser Glu Ser Phe Ala Gly Gly Asn Pro Ser Asp Gln Gln                                                                    | 1   | 5   | 15  |
|                                                                                                                                    |     | 10  |     |
| Asn Gln Lys Arg Gln Leu Gln Ile Cys Gly Pro Arg Pro Ser Pro Leu                                                                    | 20  | 25  | 30  |
|                                                                                                                                    |     | 30  |     |
| Ser Val Asn Lys Asp Ser His Lys Ile Lys Lys Pro Pro Lys His Pro                                                                    | 35  | 40  | 45  |

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Ala Pro Pro Pro Gln His Arg Asp Gln Ala Pro Leu Tyr Ala Ala Arg  
 50 55 60

Glu Pro Val Val Ile Tyr Ala Val Ser Pro Lys Val Val His Thr Thr  
 65 70 75 80

Ala Ser Asp Phe Met Asn Val Val Gln Arg Leu Thr Gly Ile Ser Ser  
 85 90 95

Ala Val Phe Leu Glu Ser Gly Asn Gly Asp Val Ser Pro Ala Ala  
 100 105 110

Arg Leu Ala Ala Thr Glu Asn Ala Ser Pro Arg Gly Gly Lys Glu Pro  
 115 120 125

Val Met Ala Ala Lys Asp Glu Thr Val Glu Ile Ala Thr Ala Met Glu  
 130 135 140

Glu Ala Ala Glu Leu Ser Gly Tyr Ala Pro Gly Ile Leu Ser Pro Ser  
 145 150 155 160

Pro Ala Met Leu Pro Thr Ala Ser Ala Gly Ile Phe Ser Gln Met Thr  
 165 170 175

Thr His Gln Gly Gly Met Phe Ser Pro Gly Leu Phe Ser Pro Ala Gly  
 180 185 190

Leu Met Ser Pro Phe Gly Phe Ala Ser Leu Val Ala Ser Pro Thr Phe  
 195 200 205

Ala Asp Leu Phe Ser His Ile Trp Gly  
 210 215

<210> 11  
 <211> 20  
 <212> DNA  
 <213> Brassica oleracea

<400> 11  
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20

<210> 12  
 <211> 20  
 <212> DNA  
 <213> Brassica oleracea

<400> 12  
 tatccccaaa tatgactgaa

20

<210> 13  
 <211> 878  
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 <213> Brassica oleracea

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<220>  
 <221> CDS  
 <222> (198)..(833)

|                                                                 |            |                                             |            |            |            |     |
|-----------------------------------------------------------------|------------|---------------------------------------------|------------|------------|------------|-----|
| <400>                                                           | 13         |                                             |            |            |            |     |
| aaaagtcaac                                                      | attttcaaag | tcaaactaat                                  | cggcttcaga | aaacaaaaat | aactttgtgt | 60  |
| gttgatgttt                                                      | aggtaatat  | actcgctcgc                                  | aaaacatccc | ttcaatttct | cagaccaaac | 120 |
| acagagaaga                                                      | aacaagttgg | atccaaactc                                  | tctacaacaa | aaagtagtga | acgagagaag | 180 |
| ctctccccaa                                                      | gcgttta    | atg gat ccg tcg gag cac ttc gcc ggc ggt aat |            |            |            | 230 |
|                                                                 |            | Met Asp Pro Ser Glu His Phe Ala Gly Gly Asn |            |            |            |     |
|                                                                 | 1          | 5                                           | 10         |            |            |     |
| cct ttc gat caa cag act cca aaa cgt cag ctt cag atc tgt ggc cct |            |                                             |            |            |            | 278 |
| Pro Phe Asp Gln Gln Thr Pro Lys Arg Gln Leu Gln Ile Cys Gly Pro |            |                                             |            |            |            |     |
|                                                                 | 15         | 20                                          | 25         |            |            |     |
| cgt cct tca cct cta agc gtc aac aaa gac tct cac aag atc aag aaa |            |                                             |            |            |            | 326 |
| Arg Pro Ser Pro Leu Ser Val Asn Lys Asp Ser His Lys Ile Lys Lys |            |                                             |            |            |            |     |
|                                                                 | 30         | 35                                          | 40         |            |            |     |
| cct ccc agg cac cct gct cca cct cct cag cat cac cgc gac caa gct |            |                                             |            |            |            | 374 |
| Pro Pro Arg His Pro Ala Pro Pro Gln His His Arg Asp Gln Ala     |            |                                             |            |            |            |     |
|                                                                 | 45         | 50                                          | 55         |            |            |     |
| ccg ctc tac cct cct cga gag ccg gtg gtt atc tac gcc gtc tcg ccg |            |                                             |            |            |            | 422 |
| Pro Leu Tyr Pro Pro Arg Glu Pro Val Val Ile Tyr Ala Val Ser Pro |            |                                             |            |            |            |     |
|                                                                 | 60         | 65                                          | 70         | 75         |            |     |
| aaa gtc gtg cac acc aca acc tcc gat ttc atg aac gtc gtc cag cgt |            |                                             |            |            |            | 470 |
| Lys Val Val His Thr Thr Ser Asp Phe Met Asn Val Val Gln Arg     |            |                                             |            |            |            |     |
|                                                                 | 80         | 85                                          | 90         |            |            |     |
| ctc acc ggg atc tcc tcc gag gtc ttc ctc gaa tca aga aac gac gga |            |                                             |            |            |            | 518 |
| Leu Thr Gly Ile Ser Ser Glu Val Phe Leu Gln Ser Arg Asn Asp Gly |            |                                             |            |            |            |     |
|                                                                 | 95         | 100                                         | 105        |            |            |     |
| gat gta tca ccg gcg gcg aga ctc gcc gcg acg gag aat gct agc ccg |            |                                             |            |            |            | 566 |
| Asp Val Ser Pro Ala Ala Arg Leu Ala Ala Thr Glu Asn Ala Ser Pro |            |                                             |            |            |            |     |
|                                                                 | 110        | 115                                         | 120        |            |            |     |
| aga gga gga aag gaa ccg gtg gaa agc tcg acg gct atg gaa gaa gca |            |                                             |            |            |            | 614 |
| Arg Gly Gly Lys Glu Pro Val Glu Ser Ser Thr Ala Met Glu Glu Ala |            |                                             |            |            |            |     |
|                                                                 | 125        | 130                                         | 135        |            |            |     |
| gct gag ttc ggt tgt tat gtg ccg gga ata ctc tcg ccg tct ccg gct |            |                                             |            |            |            | 662 |
| Ala Glu Phe Gly Cys Tyr Val Pro Gly Ile Leu Ser Pro Ser Pro Ala |            |                                             |            |            |            |     |
|                                                                 | 140        | 145                                         | 150        | 155        |            |     |
| atg tta ccg acc gtt ccc gcc gga att ttc tct ccg atg ttt cac cta |            |                                             |            |            |            | 710 |
| Met Leu Pro Thr Val Pro Ala Gly Ile Phe Ser Pro Met Phe His Leu |            |                                             |            |            |            |     |
|                                                                 | 160        | 165                                         | 170        |            |            |     |
| ggt ggg ttg ttt tcg ccg gcg ttg ccg ccg gga tta ttt tcg ccg gca |            |                                             |            |            |            | 758 |
| Gly Gly Leu Phe Ser Pro Ala Leu Pro Pro Gly Leu Phe Ser Pro Ala |            |                                             |            |            |            |     |
|                                                                 | 175        | 180                                         | 185        |            |            |     |
| gga tta atg agc cct ggt tat gct agt ttg gcg tca cca aat ttt gct |            |                                             |            |            |            | 806 |
| Gly Leu Met Ser Pro Gly Tyr Ala Ser Leu Ala Ser Pro Asn Phe Ala |            |                                             |            |            |            |     |
|                                                                 | 190        | 195                                         | 200        |            |            |     |
| gat ttc ttc agt cac att tgg gat cct tagagaatag attatttagtt      |            |                                             |            |            |            | 853 |
| Asp Phe Phe Ser His Ile Trp Asp Pro                             |            |                                             |            |            |            |     |
|                                                                 | 205        | 210                                         |            |            |            |     |

## P200301025DK SEQ listing.ST25

tttttttatta tttacatttt atgta 878

<210> 14  
<211> 212  
<212> PRT  
<213> Brassica oleracea

<400> 14

Met Asp Pro Ser Glu His Phe Ala Gly Gly Asn Pro Phe Asp Gln Gln  
1 5 10 15

Thr Pro Lys Arg Gln Leu Gln Ile Cys Gly Pro Arg Pro Ser Pro Leu  
20 25 30

Ser Val Asn Lys Asp Ser His Lys Ile Lys Lys Pro Pro Arg His Pro  
35 40 45

Ala Pro Pro Pro Gln His His Arg Asp Gln Ala Pro Leu Tyr Pro Pro  
50 55 60

Arg Glu Pro Val Val Ile Tyr Ala Val Ser Pro Lys Val Val His Thr  
65 70 75 80

Thr Thr Ser Asp Phe Met Asn Val Val Gln Arg Leu Thr Gly Ile Ser  
85 90 95

Ser Glu Val Phe Leu Glu Ser Arg Asn Asp Gly Asp Val Ser Pro Ala  
100 105 110

Ala Arg Leu Ala Ala Thr Glu Asn Ala Ser Pro Arg Gly Gly Lys Glu  
115 120 125

Pro Val Glu Ser Ser Thr Ala Met Glu Glu Ala Ala Glu Phe Gly Cys  
130 135 140

Tyr Val Pro Gly Ile Leu Ser Pro Ser Pro Ala Met Leu Pro Thr Val  
145 150 155 160

Pro Ala Gly Ile Phe Ser Pro Met Phe His Leu Gly Gly Leu Phe Ser  
165 170 175

Pro Ala Leu Pro Pro Gly Leu Phe Ser Pro Ala Gly Leu Met Ser Pro  
180 185 190

Gly Tyr Ala Ser Leu Ala Ser Pro Asn Phe Ala Asp Phe Phe Ser His  
195 200 205

Ile Trp Asp Pro  
210

<210> 15

## P200301025DK SEQ Listing.ST25

<211> 393  
<212> DNA  
<213> Glycine max

<220>  
<221> CDS  
<222> (1)..(393)

<400> 15  
caa ctt caa ggt cca cgc cct aca cct ctc aga ata aac aaa gac tct      48  
Gln Leu Gln Gly Pro Arg Pro Thr Pro Leu Arg Ile Asn Lys Asp Ser  
1                5                10                15  
cat aaa atc aag aaa cca ccg ttg gca cca caa cct tca cac cct cat      96  
His Lys Ile Lys Lys Pro Pro Leu Ala Pro Gln Pro Ser His Pro His  
20                25                30  
caa cct cca ccg cgc caa cct ata ata atc tac acc gtg tcc ccc aag      144  
Gln Pro Pro Pro Arg Gln Pro Ile Ile Ile Tyr Thr Val Ser Pro Lys  
35                40                45  
gtg att cac acc acc cca agt gac ttc atg aac ctc gtc caa cgc ctc      192  
Val Ile His Thr Thr Pro Ser Asp Phe Met Asn Leu Val Gln Arg Leu  
50                55                60  
act ggg tcc agt tct tct tcc tct gct gaa gtg gtc atg tcc aac aat      240  
Thr Gly Ser Ser Ser Ser Ser Ala Glu Val Val Met Ser Asn Asn Asn  
65                70                75                80  
aac aac acc act cat gtc gac cct ttc aac aac ggc ggc ggc gga atg      288  
Asn Asn Thr Thr His Val Asp Pro Phe Asn Asn Gly Gly Gly Met  
85                90                95  
gtg tcg ccg gcg gcg cgt tac gcc acc ata gag aag gcc atg tcc cct      336  
Val Ser Pro Ala Ala Arg Tyr Ala Thr Ile Glu Lys Ala Met Ser Pro  
100                105                110  
atg ggg aaa aaa cat gtt ctt ctt cca agt gtg aac aat att ata agc      384  
Met Gly Lys Lys His Val Leu Leu Pro Ser Val Asn Asn Ile Ile Ser  
115                120                125  
gat gtg gaa  
Asp Val Glu  
130

<210> 16  
<211> 131  
<212> PRT  
<213> Glycine max

<400> 16  
Gln Leu Gln Gly Pro Arg Pro Thr Pro Leu Arg Ile Asn Lys Asp Ser  
1                5                10                15

His Lys Ile Lys Lys Pro Pro Leu Ala Pro Gln Pro Ser His Pro His  
20                25                30

Gln Pro Pro Pro Arg Gln Pro Ile Ile Ile Tyr Thr Val Ser Pro Lys  
35                40                45

Val Ile His Thr Thr Pro Ser Asp Phe Met Asn Leu Val Gln Arg Leu  
50                55                60

## P200301025DK SEQ listing.ST25

Thr Gly Ser Ser Ser Ser Ser Ala Glu Val Val Met Ser Asn Asn  
 65                    70                    75                    80

Asn Asn Thr Thr His Val Asp Pro Phe Asn Asn Gly Gly Gly Met  
 85                    90                    95

Val Ser Pro Ala Ala Arg Tyr Ala Thr Ile Glu Lys Ala Met Ser Pro  
 100                    105                    110

Met Gly Lys Lys His Val Leu Leu Pro Ser Val Asn Asn Ile Ile Ser  
 115                    120                    125

Asp Val Glu  
 130

<210> 17  
<211> 19  
<212> DNA  
<213> Glycine max

<400> 17  
ccatagagaa ggccatgtc

19

<210> 18  
<211> 20  
<212> DNA  
<213> Glycine max

<400> 18  
tgaatgttgt ggtgccaacg

20

<210> 19  
<211> 927  
<212> DNA  
<213> Oryza sp.

<220>  
<221> CDS  
<222> (7)..(927)

<400> 19  
gtggcg atg gaa ttc ccg tcg tcg acg tcg ccg tcg ccg tcg ccg tcg  
 Met Glu Phe Pro Ser Ser Thr Ser Pro Ser Pro Ser Pro Ser  
 1                5                10

48

tcc ggg cag cat cag cag ccg acg acg ccg ccg ccg ctt cag  
 Ser Gly Gln His Gln Gln Pro Thr Thr Pro Arg Arg Gln Leu Gln  
 15                20                25                30

96

ggc ccg cgc ccc ccg cggtt ctc aac gtg ccg atg gag tcg cac gcc atc  
 Gly Pro Arg Pro Arg Leu Asn Val Arg Met Glu Ser His Ala Ile  
 35                40                45

144

aag aag ccg tcg tcc ggg gcg gcc gcg gcg gcg gcg gcg cag gcg  
 Lys Lys Pro Ser Ser Gly Ala Ala Ala Ala Ala Ala Ala Gln Ala  
 50                55                60

192

agg cgg gag cag cag ccg ccg cgg gcg ccg gtg atc atc tac

240

P200301025DK SEQ listing\_ST25  
 Arg Arg Glu Gln Gln Gln Pro Pro Pro Arg Ala Pro Val Ile Ile Tyr  
 65 70 75

|                                                                                                                                                      |     |
|------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| gac gcg tcg ccg aag att atc cac gcc aag ccc aac gag ttc atg gcg<br>Asp Ala Ser Pro Lys Ile Ile His Ala Lys Pro Asn Glu Phe Met Ala<br>80 85 90       | 288 |
| ctc gtg cag cgg ctc acc ggc ccg ggg tcg ggg ccg ccg gcg ccg ccg<br>Leu Val Gln Arg Leu Thr Gly Pro Gly Ser Gly Pro Pro Ala Pro Pro<br>95 100 105 110 | 336 |
| cat caa ggg gag gcc cag gcg cag gac tac ccg atg atg gac gag gcc<br>His Gln Gly Glu Ala Gln Ala Gln Asp Tyr Pro Met Met Asp Glu Ala<br>115 120 125    | 384 |
| gcc gcg cag cag ttc ttc ccg ccg gag ctg ctg ctc tcg ccg tcg gcc<br>Ala Ala Gln Gln Phe Phe Pro Pro Glu Leu Leu Leu Ser Pro Ser Ala<br>130 135 140    | 432 |
| gcg atg tcc ccg gcg agg ctg gcg acc atc gag agg tcc gtc cgc<br>Ala Met Ser Pro Ala Ala Arg Leu Ala Thr Ile Glu Arg Ser Val Arg<br>145 150 155        | 480 |
| ccg atg ccc gag ccg gcg ccg gag tac gtg gac atc acg aac ggc ggc<br>Pro Met Pro Glu Pro Ala Pro Glu Tyr Val Asp Ile Thr Asn Gly Gly<br>160 165 170    | 528 |
| ggc ggc ggg gtc gac gac ggc ctc gcg gcg atc ctc ggc tcg<br>Gly Gly Gly Val Asp Asp Gly Gly Leu Ala Ala Ile Leu Gly Ser<br>175 180 185 190            | 576 |
| atc cgg cca ggc atc ctc tcc ccg ctc ccc tcc tcc ctc ccg ccc gcc<br>Ile Arg Pro Gly Ile Leu Ser Pro Leu Pro Ser Ser Leu Pro Pro Ala<br>195 200 205    | 624 |
| gcc gtc ccc ggc cag ttc tcg ccg ctc ccg ttc gac gcg agg ccg ctc<br>Ala Val Pro Gly Gln Phe Ser Pro Leu Pro Phe Asp Ala Arg Pro Leu<br>210 215 220    | 672 |
| ccg ttc gac gcg agc tgc atc agc tgg ctc aac gag ctg agc ccc atc<br>Pro Phe Asp Ala Ser Cys Ile Ser Trp Leu Asn Glu Leu Ser Pro Ile<br>225 230 235    | 720 |
| ctc cgg gcc gcc tcc gcc ggc gcg gcc tcg tcc ggc agc ggc ggc ggc<br>Leu Arg Ala Ala Ser Ala Gly Ala Ala Ser Ser Gly Ser Gly Gly Gly<br>240 245 250    | 768 |
| ggc agc ggt ggc aac acc agc aac ggc ggc ggc gcc cgc ccg ccg ccg<br>Gly Ser Gly Gly Asn Thr Ser Asn Gly Gly Ala Arg Pro Pro Pro<br>255 260 265 270    | 816 |
| tcc tac tac gcc gac cca ttc gtc ccc agc cca cgt cac ctc ctc gcc<br>Ser Tyr Tyr Ala Asp Pro Phe Val Pro Ser Pro Arg His Leu Leu Ala<br>275 280 285    | 864 |
| acg ccc acc gtg ccg tcg ccg gcg acc tgc gcc gag ctc ttc agc aac<br>Thr Pro Thr Val Pro Ser Pro Ala Thr Cys Ala Glu Leu Phe Ser Asn<br>290 295 300    | 912 |
| ctg ccg gat ctc tag<br>Leu Pro Asp Leu<br>305                                                                                                        | 927 |

<210> 20  
 <211> 306  
 <212> PRT  
 <213> Oryza sp.

## P200301025DK SEQ listing.ST25

&lt;400&gt; 20

Met Glu Phe Pro Ser Ser Thr Ser Pro Ser Pro Ser Pro Ser Ser Gly  
 1 5 10 15

Gln His Gln Gln Gln Pro Thr Thr Pro Arg Arg Gln Leu Gln Gly Pro  
 20 25 30

Arg Pro Pro Arg Leu Asn Val Arg Met Glu Ser His Ala Ile Lys Lys  
 35 40 45

Pro Ser Ser Gly Ala Ala Ala Ala Ala Ala Ala Gln Ala Arg Arg  
 50 55 60

Glu Gln Gln Gln Pro Pro Pro Arg Ala Pro Val Ile Ile Tyr Asp Ala  
 65 70 75 80

Ser Pro Lys Ile Ile His Ala Lys Pro Asn Glu Phe Met Ala Leu Val  
 85 90 95

Gln Arg Leu Thr Gly Pro Gly Ser Gly Pro Pro Ala Pro Pro His Gln  
 100 105 110

Gly Glu Ala Gln Ala Gln Asp Tyr Pro Met Met Asp Glu Ala Ala Ala  
 115 120 125

Gln Gln Phe Phe Pro Pro Glu Leu Leu Leu Ser Pro Ser Ala Ala Met  
 130 135 140

Ser Pro Ala Ala Arg Leu Ala Thr Ile Glu Arg Ser Val Arg Pro Met  
 145 150 155 160

Pro Glu Pro Ala Pro Glu Tyr Val Asp Ile Thr Asn Gly Gly Gly  
 165 170 175

Gly Gly Val Asp Asp Gly Gly Leu Ala Ala Ile Leu Gly Ser Ile Arg  
 180 185 190

Pro Gly Ile Leu Ser Pro Leu Pro Ser Ser Leu Pro Pro Ala Ala Val  
 195 200 205

Pro Gly Gln Phe Ser Pro Leu Pro Phe Asp Ala Arg Pro Leu Pro Phe  
 210 215 220

Asp Ala Ser Cys Ile Ser Trp Leu Asn Glu Leu Ser Pro Ile Leu Arg  
 225 230 235 240

Ala Ala Ser Ala Gly Ala Ala Ser Ser Gly Ser Gly Gly Gly Ser  
 245 250 255

Gly Gly Asn Thr Ser Asn Gly Gly Ala Arg Pro Pro Pro Ser Tyr

P200301025DK SEQ listing.ST25  
265 270

Tyr Ala Asp Pro Phe Val Pro Ser Pro Arg His Leu Leu Ala Thr Pro  
275 280 285

Thr Val Pro Ser Pro Ala Thr Cys Ala Glu Leu Phe Ser Asn Leu Pro  
290 295 300

Asp Leu  
305

<210> 21  
<211> 16  
<212> DNA  
<213> *Oryza* sp.

<400> 21  
atggaaattcc cgtcgt 16

<210> 22  
<211> 19  
<212> DNA  
<213> *Oryza* sp.

<400> 22 ctagagatcc ggcagggttg 19

<210> 23  
<211> 781  
<212> DNA  
<213> CaMV 35S promoter duplicated

<400> 23  
atggtgtggagc acgacactct cgtctactcc aagaatatca aagatacagt ctcagaagac 60  
caaagggcta tttagacttt tcaacaaagg gtaatatcg gaaacctcct cgattccat 120  
tgcccagcta tctgtcactt catcaaaagg acagtagaaa aggaagggtgg cacctacaaa 180  
tgcccatcatt gcgataaaagg aaaggctatc gttcaagatg cctctgccga cagtggtccc 240  
aaagatggac cccccccac gaggagcatc gtggaaaaag aagacgttcc aaccacgtct 300  
tcaaagcaag tggattgatg tgataacatg gtggagcacg acactctcg tctactccaag 360  
aatatcaaag atacagtctc agaagaccaa agggctattg agactttca acaaagggtta 420  
atatcgggaa acctcctcgg attccattgc ccagctatct gtcacttcat caaaaggaca 480  
gtagaaaaagg aaggtggcac ctacaaatgc catcattgcg ataaaaggaaa ggctatcg 540  
caagatgcct ctggccgacag tggtcccaa gatggacccc cacccacgag gagcatcg 600  
gaaaaagaag acgttccaaac cacgtcttca aagcaagtgg attgatgtga tatctccact 660  
gacgtaaggg atgacgcaca atcccactat cttcgcaag accttcctct atataaggaa 720  
gttcatttca tttggagagg acacgctgaa atcaccagtc tctctctaca aatctatctc 780  
t 781

## P200301025DK SEQ listing.ST25

<210> 24  
<211> 253  
<212> DNA  
<213> Agrobacterium NOS terminator

<400> 24  
cgttcaaaca tttggcaata aagtttctta agattgaatc ctgttgccgg tcttgcgatg 60  
attatcatat aatttctgtt gaattacgtt aagcatgtaa taattaacat gtaatgcgt 120  
acgttattta tgagatgggt ttttatgatt agagtcccgc aattatacat ttaatacgcg 180  
atagaaaaca aaatatagcg cgcaaactag gataaattat cgcgcggt gtcatctatg 240  
ttactagatc ggg 253

<210> 25  
<211> 189  
<212> DNA  
<213> Synthetic intron

<400> 25  
gtaagtttct gcttctacct ttgatataataataatt atcattaatt agtagtaata 60  
taatatttca aatatttttt tcaaaataaa agaatgtagt atatagcaat tgctttctg 120  
tagttataaa gtgtgtatat tttaatttat aactttcta atatatgacc aaaatttgtt 180  
gatgtgcag 189

<210> 26  
<211> 207  
<212> PRT  
<213> Oryza sp.

<400> 26

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Gln | Gln | Leu | Ser | Ser | Pro | Ser | Ala | Ser | Gln | Arg | Gly | Gly | Gly |
| 1   |     |     |     | 5   |     |     |     |     |     |     | 10  |     |     |     | 15  |

Arg Glu Leu Gln Gly Pro Arg Pro Ala Pro Leu Lys Val Arg Lys Glu  
20 25 30

Ser His Lys Ile Arg Lys Gln Glu Pro Val Gln Gln Leu Arg Gln Pro  
35 40 45

Val Ile Ile Tyr Thr Met Ser Pro Lys Val Val His Ala Asn Ala Ala  
50 55 60

Asp Phe Met Ser Val Val Gln Arg Leu Thr Gly Ala Pro Pro Thr Ala  
65 70 75 80

Pro Pro Gln Pro Gln Pro His His Pro Thr Leu Leu Ala Gln Met Pro  
85 90 95

Pro Gln Pro Ser Phe Pro Phe His Leu Gln Gln Gln Asp Ala Trp Pro  
100 105 110

Gln Gln Gln His Ser Pro Ala Ala Ile Glu Gln Ala Ala Ala Arg Ser

P200301025DK SEQ listing.ST25  
 115                   120                   125

Ser Gly Ala Asp Leu Pro Pro Leu Pro Ser Ile Leu Ser Pro Val Pro  
 130                   135                   140

Gly Thr Val Leu Pro Ala Ile Pro Ala Ser Phe Phe Ser Pro Pro Ser  
 145                   150                   155                   160

Leu Ile Ser Pro Val Pro Phe Leu Gly Ala Thr Thr Thr Ser Ser Ala  
 165                   170                   175

Ala Pro Ser Thr Ser Pro Ser Pro Met Gly Gly Ser Ala Tyr Tyr Trp  
 180                   185                   190

Asp Leu Phe Asn Met Gln Gln Gln His Tyr His His Gln Asn  
 195                   200                   205

<210> 27  
<211> 238  
<212> PRT  
<213> Zea mays

<400> 27

Met Asp Pro Pro Ser Ser Ser Gly Arg Pro Thr Thr Pro Arg Arg Gln  
 1                   5                   10                   15

Leu Gln Gly Pro Arg Pro Pro Arg Leu Asn Val Arg Met Glu Ser His  
 20                   25                   30

Ala Ile Lys Lys Pro Ser Ala Ser Gly Ala Pro Pro Ala Pro Gly Gln  
 35                   40                   45

Gly Arg Pro Arg Asp His His His His Pro Gln Pro Gly Arg Ala  
 50                   55                   60

Pro Val Ile Ile Tyr Asp Ala Ser Pro Lys Val Ile His Ala Lys Pro  
 65                   70                   75                   80

Ser Glu Phe Met Ala Leu Val Gln Arg Leu Thr Gly Pro Gly Ala Gln  
 85                   90                   95

Ala Gln His Glu Arg His Val Ala Asp Asp Asp Ala Thr Ala Asn Gly  
 100                   105                   110

Gly Gly Val Leu Gly Gln Ala Phe Leu Pro Pro Glu Leu Leu Leu Ser  
 115                   120                   125

Pro Ser Ala Ala Met Ser Pro Ala Ala Arg Leu Ala Thr Ile Glu Arg  
 130                   135                   140

Ser Val Arg Pro Val Pro Ala Pro Ala Pro Ala Pro Asp Tyr Ala Ala  
 145                   150                   155                   160

## P200301025DK SEQ Listing.ST25

Asp Gly His Pro Arg Gly Gly Ala Arg Pro Arg Glu Ala Pro Arg His  
 165 170 175

Pro Val Pro Ala Ala Val Leu Ala Ala Gly Arg Arg Val Gly Pro  
 180 185 190

Val Leu Ala Ala Ala Leu Arg Pro Gln Gln Arg Gln Leu Ala Gln Arg  
 195 200 205

Ala Gln Pro His Pro Pro Gly Ser Val His Gly Gln Arg Ser Ala Pro  
 210 215 220

Leu Ala His Ala His Gly Pro Thr Gly Gly Ser Arg Gln Pro  
 225 230 235

<210> 28  
 <211> 271  
 <212> PRT  
 <213> Zea mays

<400> 28

Gln Gly Pro Arg Pro Pro Arg Leu Ala Val Ser Lys Asp Ser His Lys  
 1 5 10 15

Val Arg Lys Pro Pro Val Ala Pro Gln Arg Gln Gln His Gln His Gln  
 20 25 30

Gln Pro Ala Ala Gln Leu Gln Gln Gln His Gln Tyr His Gln Gln  
 35 40 45

Gln Gln Gln Gln Gly Arg Gln Pro Val Ile Ile Tyr Asp Ala Ser Pro  
 50 55 60

Lys Val Ile His Thr Lys Pro Gly Asp Phe Met Ala Leu Val Gln Arg  
 65 70 75 80

Leu Thr Gly Pro Gly Ser Thr Ser Gln Ala Gln Phe Asp Ala Ala Ala  
 85 90 95

Ala Ala Ala Gly Pro Ser His Pro Ala Ala Met Glu Phe Glu Pro Arg  
 100 105 110

Glu Phe Leu Leu Ser Pro Thr Ala Ala Leu Ser Pro Ala Ala Arg Leu  
 115 120 125

Ala Ala Ile Glu Arg Ser Val Arg Pro Leu Pro Pro His His Ala Pro  
 130 135 140

Ala Ala Val Pro Pro Tyr Phe Gly Ala Thr Asn Asp Asp Gly Phe Phe  
 145 150 155 160

## P200301025DK SEQ listing.ST25

Leu Pro Gly Ser Ala Asp Met Asp Ser Leu Ser Ala Ala Leu Gly Pro  
165 170 175

Pro Ala Gly Arg Pro Gly Ile Leu Ser Pro Ala Ala Leu Pro Pro Ala  
180 185 190

Ala Ser Thr Gly Leu Phe Ser Pro Met Pro Phe Asp Pro Ser Cys Leu  
195 200 205

Ser Trp Leu Ser Glu Leu Ser Pro Phe Leu Pro Ser Ala Gly Thr Arg  
210 215 220

Ala Ala Ala Ala Gly Leu Leu Asp Gln Ala Pro Phe Ala Pro Ser Pro  
225 230 235 240

Arg Ser Ser Leu Leu Leu Ser Thr Pro Thr Met Pro Ser Pro Ala Thr  
245 250 255

Phe Ser Val Leu Glu Phe Phe Ser Ser Pro Asn Phe Pro Asp Leu  
260 265 270